

1/2/02
A-378CIP5.ST25.txt
SEQUENCE LISTING

<110> BOYLE, WILLIAM J.
LACEY, DAVID LEE
CALZONE, FRANK J.
CHANG, MING-SHI
SENALDI, GIORGIO

<120> COMBINATION THERAPY FOR CONDITIONS LEADING TO BONE LOSS

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<140> US 09/613,591
<141> 2000-07-10

<150> US 09/457,647
<151> 1999-12-09

<150> US 09/350,670
<151> 1999-07-09

<150> US 08/706,945
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 <210> 83
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<210> 86
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<210> 88
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<400> 88
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<210> 93
<211> 26
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<220>
<223> pAMG21-huOPG

<400> 93
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<210> 94
<211> 50
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<223> pAMG21-huOPG

<400> 94
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<210> 98
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<400> 103
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<210> 104
 <211> 59
 <212> DNA
 <213> Homo sapiens

<400> 104
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 <212> DNA
 <213> Homo sapiens

<400> 105
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<210> 106
 <211> 31
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 <213> Homo sapiens

<400> 106
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<210> 107
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<220>
 <223> PCR primer for Fc-hOPG fusion protein.

<400> 107
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<210> 108
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>

<223> PCR primer for FchOPG fusion protein.

<400> 108
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<210> 109
<211> 45
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<220>
<223> Fc/muOPG

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<210> 112
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<400> 113
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<210> 114
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<212> DNA
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<220>
<223> pAMG21-huOPG

<220>
<221> misc_feature
<223> Linker with XbaI and KpnI sites inserted into human sequence.

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<223> huOPG

<400> 116
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ttggagcaaa agtttccata tgttattcct cctt 94

<210> 117
<211> 62
<212> DNA
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<400> 117
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aa 62

<210> 118
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

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tt

62

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 <213> Homo sapiens

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Asp Thr Val Cys His Lys Pro Cys Glu Pro Gly Val Thr Tyr Thr Asp
 35 40 45

Asp Trp His
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aca atg aac aag tgg ctg tgc tgt gca ctc ctg gtg ttc ttg gac atc 168
 Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile
 1 5 10 15

att gaa tgg aca acc cag gaa acc ttt cct cca aaa tac ttg cat tat 216
 Ile Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr
 20 25 30

gac cca gaa acc gga cgt cag ctc ttg tgt gac aaa tgt gct cct ggc 264
 Asp Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly
 35 40 45

acc tac cta aaa cag cac tgc aca gtc agg agg aag aca ctg tgt gtc 312
 Thr Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val
 50 55 60

cct tgc cct gac tac tct tat aca gac agc tgg cac acg agt gat gaa 360
 Pro Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu
 65 70 75

tgc gtg tac tgc agc ccc gtg tgc aag gaa ctg cag acc gtg aaa cag 408
 Cys Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln
 80 85 90 95

gag tgc aac cgc acc cac aac cga gtg tgc gaa tgt gag gaa ggg cgc 456
 Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg

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Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	Gly	Glu	Thr	Ser	Ser	Lys	Ala	Pro			
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Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	Ser	Leu	Gly	Leu	Leu	Leu	Ile	Gln			
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Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Val	Cys	Ser	Gly	Asn	Arg	Glu	Ala			
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act	caa	aat	tgt	gaa	ata	gat	gtc	acc	ctg	tgc	gaa	gag	gca	ttc	ttc	744		
Thr	Gln	Asn	Cys	Glu	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe			
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Arg	Phe	Ala	Val	Pro	Thr	Lys	Ile	Ile	Pro	Asn	Trp	Leu	Ser	Val	Leu			
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gtg	gac	agt	ttg	cct	ggg	acc	aaa	gtg	aat	gca	gag	agt	gta	gag	agg	840		
Val	Asp	Ser	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg			
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ata	aaa	cgg	aga	cac	agc	tcg	caa	gag	caa	act	ttc	cag	cta	ctt	aag	888		
Ile	Lys	Arg	Arg	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys			
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Gln	Asp	Ile	Asp	Leu	Cys	Glu	Ser	Ser	Val	Gln	Arg	His	Ile	Gly	His			
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Ala	Asn	Leu	Thr	Thr	Glu	Gln	Leu	Arg	Ile	Leu	Met	Glu	Ser	Leu	Pro			
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320					325					330					335			
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Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met	Tyr	Ala	Leu	Lys	His			
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ttg	aaa	gca	tac	cac	ttt	ccc	aaa	acc	gtc	acc	cac	agt	ctg	agg	aag	1224		
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370

375

380

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385 390 395

tgc tta tagttaggaa tggctactgg gctgtttctt caggatgggc caacactgat 1376
Cys Leu
400

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<210> 121
 <211> 401
 <212> PRT
 <213> Rattus rattus

<400> 121

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Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile
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20 25 30

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Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
35 40 45

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Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
50 55 60

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Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 65 70 75 80
 Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu
 85 90 95
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
 100 105 110
 Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu
 115 120 125
 Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 130 135 140
 Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
 145 150 155 160
 Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys
 165 170 175
 Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr
 180 185 190
 Gln Asn Cys Glu Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
 195 200 205
 Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val
 210 215 220
 Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 225 230 235 240
 Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
 245 250 255
 Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln
 260 265 270
 Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His Ala
 275 280 285
 Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro Gly
 290 295 300
 Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys
 305 310 315 320
 Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
 325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu
 340 345 350

Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr
 355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu
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Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
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Leu

<210> 122
 <211> 1325
 <212> DNA
 <213> Mus musculus

<220>
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 <222> (91)..(1293)
 <223>

<220>
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 <222> (11)..(11)
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 Met Asn Lys Trp Leu Cys Cys Ala
 1 5

ctc ctg gtg ctc ctg gac atc att gaa tgg aca acc cag gaa acc ctt 162
 Leu Leu Val Leu Leu Asp Ile Ile Glu Trp Thr Thr Gln Glu Thr Leu
 10 15 20

ctt cca aag tac ttg cat tat gac cca gaa act ggt cat cag ctc ctg 210
 Leu Pro Lys Tyr Leu His Tyr Asp Pro Glu Thr Gly His Gln Leu Leu
 25 30 35 40

tgt gac aaa tgt gct cct ggc acc tac cta aaa cag cac tgc aca gtg 258
 Cys Asp Lys Cys Ala Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Val
 45 50 55

agg agg aag aca ttg tgt gtc cct tgc cct gac cac tct tat acg gac 306
 Arg Arg Lys Thr Leu Cys Val Pro Cys Pro Asp His Ser Tyr Thr Asp
 60 65 70

agc tgg cac acc agt gat gag tgt gtg tat tgc agc cca gtg tgc aag 354
 Ser Trp His Thr Ser Asp Glu Cys Val Tyr Cys Ser Pro Val Cys Lys
 75 80 85

gaa ctg cag tcc gtg aag cag gag tgc aac cgc acc cac aac cga gtg 402
 Glu Leu Gln Ser Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val

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gag cga aac aca gtt tgc aaa aaa tgt cca gat ggg ttc ttc tca ggt Glu Arg Asn Thr Val Cys Lys Lys Cys Pro Asp Gly Phe Phe Ser Gly 140 145 150			546
gag act tca tcg aaa gca ccc tgt ata aaa cac acg aac tgc agc aca Glu Thr Ser Ser Lys Ala Pro Cys Ile Lys His Thr Asn Cys Ser Thr 155 160 165			594
ttt ggc ctc ctg cta att cag aaa gga aat gca aca cat gac aac tgt Phe Gly Leu Leu Leu Ile Gln Lys Gly Asn Ala Thr His Asp Asn Cys 170 175 180			642
tgt tcc gga aac aga gaa gcc acg caa aag tgt gga ata gat gtc acc Cys Ser Gly Asn Arg Glu Ala Thr Gln Lys Cys Gly Ile Asp Val Thr 185 190 195 200			690
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cca aat tgg ctg agt gtt ttg gtg gac agt ttg cct ggg acc aaa gtg Pro Asn Trp Leu Ser Val Leu Val Asp Ser Leu Pro Gly Thr Lys Val 220 225 230			786
aat gcc gag agt gta gag agg ata aaa cgg aga cac agc tca caa gag Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Arg His Ser Gln Glu 235 240 245			834
caa acc ttc cag ctg ctg aag ctg tgg aaa cat caa aac aga gac cag Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Arg Asp Gln 250 255 260			882
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gcc ttg atg gag agc ctg cct ggg aag aag atc agc cca gaa gag att Ala Leu Met Glu Ser Leu Pro Gly Lys Lys Ile Ser Pro Glu Glu Ile 300 305 310			1026
gag aga acg aga aag acc tgc aaa tcg agc gag cag ctc ctg aag cta Glu Arg Thr Arg Lys Thr Cys Lys Ser Ser Glu Gln Leu Leu Lys Leu 315 320 325			1074
ctc agt tta tgg agg atc aaa aat ggt gac caa gac acc ttg aag ggc Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly 330 335 340			1122
ctg atg tat gcc ctc aag cac ttg aaa aca tcc cac ttt ccc aaa act Leu Met Tyr Ala Leu Lys His Leu Lys Thr Ser His Phe Pro Lys Thr 345 350 355 360			1170
gtc acc cac agt ctg agg aag acc atg agg ttc ctg cac agc ttc aca Val Thr His Ser Leu Arg Lys Thr Met Arg Phe Leu His Ser Phe Thr			1218

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365                                370                                375
atg tac aga ctg tat cag aag ctc ttt tta gaa atg ata ggg aat cag      1266
Met Tyr Arg Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln
380                                385                                390

gtt caa tcc gtg aaa ata agc tgc tta taactaggaa tggtcactgg      1313
Val Gln Ser Val Lys Ile Ser Cys Leu
395                                400

gctgtttctt ca      1325

<210> 123
<211> 401
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<222> (11)..(11)
<223> At position 11, R is a purine.

<400> 123

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Leu Leu Asp Ile Ile
1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Leu Leu Pro Lys Tyr Leu His Tyr Asp
20 25 30

Pro Glu Thr Gly His Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
50 55 60

Cys Pro Asp His Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Ser Val Lys Gln Glu
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser
115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys
130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160

Ile Lys His Thr Asn Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys
165 170 175

```

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Gly Asn Ala Thr His Asp Asn Cys Cys Ser Gly Asn Arg Glu Ala Thr
180 185 190
Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
195 200 205
Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val
210 215 220
Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
225 230 235 240
Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
245 250 255
Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln
260 265 270
Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Leu Gly His Ser
275 280 285
Asn Leu Thr Thr Glu Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly
290 295 300
Lys Lys Ile Ser Pro Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys
305 310 315 320
Ser Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
325 330 335
Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu
340 345 350
Lys Thr Ser His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr
355 360 365
Met Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu
370 375 380
Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
385 390 395 400

Leu

<210> 124
<211> 1356
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

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<222>    (95) .. (1297)
<223>
```

```
<220>
<221> misc_feature
<222> (63)..(63)
<223> At position 63, Y is a pyrimidine.
```

<400> 124																
gtatatataa		cgtgatgagc		gtacgggtgc		ggagacgcac		cggcgcgctc		gccagccgc						60
cgycaccaag		cccctgaggt		ttccggggac		caca		atg	aac	aag	ttg	ctg	tgc	tgc		115
								Met	Asn	Lys	Leu	Leu	Cys	Cys		
								1				5				
gcg	ctc	gtg	ttt	ctg	gac	atc	tcc	att	aag	tgg	acc	acc	cag	gaa	acg	163
Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	Lys	Trp	Thr	Thr	Gln	Glu	Thr	
		10				15						20				
ttt	cct	cca	aag	tac	ctt	cat	tat	gac	gaa	gaa	acc	tct	cat	cag	ctg	211
Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	Glu	Glu	Thr	Ser	His	Gln	Leu	
		25				30				35						
ttg	tgt	gac	aaa	tgt	cct	cct	ggg	acc	tac	cta	aaa	caa	cac	tgt	aca	259
Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	
		40		45						50				55		
gca	aag	tgg	aag	tcc	gtg	tgc	gcc	cct	tgc	cct	gac	cac	tac	tac	aca	307
Ala	Lys	Trp	Lys	Ser	Val	Cys	Ala	Pro	Cys	Pro	Asp	His	Tyr	Tyr	Thr	
				60				65						70		
gac	agc	tgg	cac	acc	agt	gac	gag	tgt	cta	tac	tgc	agc	ccc	gtg	tgc	355
Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	Pro	Val	Cys	
				75				80				85				
aag	gag	ctg	cag	tac	gtc	aag	cag	gag	tgc	aat	cgc	acc	cac	aac	cgc	403
Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg	
		90				95						100				
gtg	tgc	gaa	tgc	aag	gaa	ggg	cgc	tac	ctt	gag	ata	gag	ttc	tgc	ttg	451
Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	
		105				110				115						
aaa	cat	agg	agc	tgc	cct	cct	gga	ttt	gga	gtg	gtg	caa	gct	gga	acc	499
Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr	
		120		125						130				135		
cca	gag	cga	aat	aca	gtt	tgc	aaa	aga	tgt	cca	gat	ggg	ttc	ttc	tca	547
Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	
				140				145						150		
aat	gag	acg	tca	tct	aaa	gca	ccc	tgt	aga	aaa	cac	aca	aat	tgc	agt	595
Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	
		155						160				165				
gtc	ttt	ggg	ctc	ctg	cta	act	cag	aaa	gga	aat	gca	aca	cac	gac	aac	643
Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	
		170				175						180				
ata	tgt	tcc	gga	aac	agt	gaa	tca	act	caa	aaa	tgt	gga	ata	gat	gtt	691
Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val	
		185				190				195						
acc	ctg	tgt	gag	gag	gca	ttc	ttc	agg	ttt	gct	gta	cct	aca	aag	ttt	739
Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe							

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acg cct aac tgg ctt agt gtc ttg gta gac aat ttg cct ggc acc aaa	787
Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys	
220 225 230	
gta aac gca gag agt gta gag agg ata aaa cgg caa cac agc tca caa	835
Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln	
235 240 245	
gaa cag act ttc cag ctg ctg aag tta tgg aaa cat caa aac aaa gcc	883
Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Ala	
250 255 260	
caa gat ata gtc aag aag atc atc caa gat att gac ctc tgt gaa aac	931
Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn	
265 270 275	
agc gtg cag cgg cac att gga cat gct aac ctc acc ttc gag cag ctt	979
Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu	
280 285 290 295	
cgt agc ttg atg gaa agc tta ccg gga aag aaa gtg gga gca gaa gac	1027
Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp	
300 305 310	
att gaa aaa aca ata aag gca tgc aaa ccc agt gac cag atc ctg aag	1075
Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys	
315 320 325	
ctg ctc agt ttg tgg cga ata aaa aat ggc gac caa gac acc ttg aag	1123
Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys	
330 335 340	
ggc cta atg cac gca cta aag cac tca aag acg tac cac ttt ccc aaa	1171
Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys	
345 350 355	
act gtc act cag agt cta aag aag acc atc agg ttc ctt cac agc ttc	1219
Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe	
360 365 370 375	
aca atg tac aaa ttg tat cag aag tta ttt tta gaa atg ata ggt aac	1267
Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn	
380 385 390	
cag gtc caa tca gta aaa ata agc tgc tta taactggaaa tggccattga	1317
Gln Val Gln Ser Val Lys Ile Ser Cys Leu	
395 400	
gctgtttcct cacaattggc gagatcccat ggatgataa	1356

<210> 125
 <211> 401
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (63)..(63)
 <223> At position 63, Y is a pyrimidine.

<400> 125

Met	Asn	Lys	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile
1				5					10					15	

A-378CIP5.ST25.txt

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 20 25 30

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 35 40 45

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Ser Val Cys Ala Pro
 50 55 60

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 65 70 75 80

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
 85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
 100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
 115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 130 135 140

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
 145 150 155 160

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
 165 170 175

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
 180 185 190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
 195 200 205

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
 210 215 220

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 225 230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
 245 250 255

Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln
 260 265 270

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala
 275 280 285

A-378CIP5.ST25.txt

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
290 295 300

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
305 310 315 320

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
340 345 350

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr
355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu
370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
385 390 395 400

Leu

<210> 126
<211> 139
<212> PRT
<213> Homo sapiens
<400> 126

Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys
1 5 10 15

Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
20 25 30

Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala
35 40 45

Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys
50 55 60

Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr
65 70 75 80

Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn
85 90 95

Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His
100 105 110

Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly
Page 34

115

120

125

Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys
 130 135

<210> 127
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> huOPG

<400> 127
 acctacttct ttgaagagta gtcgacgaca cactatttac aggcggcc

48

<210> 128
 <211> 219
 <212> PRT
 <213> Rattus rattus

<400> 128

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
 1 5 10 15

Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
 20 25 30

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
 35 40 45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
 50 55 60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
 65 70 75 80

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
 85 90 95

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
 100 105 110

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
 115 120 125

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
 130 135 140

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
 145 150 155 160

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
 165 170 175

Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
 180 185 190

Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
 195 200 205

Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr
 210 215

<210> 129
 <211> 281
 <212> PRT
 <213> Rattus rattus

<400> 129

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
 1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
 20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
 35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
 50 55 60

Gly Thr Tyr Leu Thr Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr
 65 70 75 80

Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His
 85 90 95

Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln
 100 105 110

Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys
 115 120 125

Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys
 130 135 140

Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln
 145 150 155 160

Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg
 165 170 175

Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys
 180 185 190

A-378CIP5.ST25.txt

```

Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp
    195                      200                205

Ser Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys
    210                      215                220

Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Thr Arg Thr Gln Arg Trp
    225                      230                235                240

Lys Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
    245                      250                255

Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro
    260                      265                270

Ser Phe Ser Pro Thr Pro Gly Phe Thr
    275                      280

<210> 130
<211> 207
<212> PRT
<213> Rattus rattus

<400> 130

Met Leu Arg Leu Ile Ala Leu Leu Val Cys Val Val Tyr Val Tyr Gly
 1      5      10      15

Asp Asp Val Pro Tyr Ser Ser Asn Gln Gly Lys Cys Gly Gly His Asp
    20      25      30

Tyr Glu Lys Asp Gly Leu Cys Cys Ala Ser Cys His Pro Gly Phe Tyr
    35      40      45

Ala Ser Arg Leu Cys Gly Pro Gly Ser Asn Thr Val Cys Ser Pro Cys
    50      55      60

Glu Asp Gly Thr Phe Thr Ala Ser Thr Asn His Ala Pro Ala Cys Val
    65      70      75      80

Ser Cys Arg Gly Pro Cys Thr Gly His Leu Ser Glu Ser Gln Pro Cys
    85      90      95

Asp Arg Thr His Asp Arg Val Cys Asn Cys Ser Thr Gly Asn Tyr Cys
    100     105     110

Leu Leu Lys Gly Gln Asn Gly Cys Arg Ile Cys Ala Pro Gln Thr Lys
    115     120     125

Cys Pro Ala Gly Tyr Gly Val Ser Gly His Thr Arg Ala Gly Asp Thr
    130     135     140

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A-378CIP5.ST25.txt

Leu Cys Glu Lys Cys Pro Pro His Thr Tyr Ser Asp Ser Leu Ser Pro
145 150 155 160

Thr Glu Arg Cys Gly Thr Ser Phe Asn Tyr Ile Ser Val Gly Phe Asn
165 170 175

Leu Tyr Pro Val Asn Glu Thr Ser Cys Thr Thr Thr Ala Gly His Asn
180 185 190

Glu Val Ile Lys Thr Lys Glu Phe Thr Val Thr Leu Asn Tyr Thr
195 200 205

<210> 131
<211> 227
<212> PRT
<213> Rattus rattus

<400> 131

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Thr Thr Asp Gln
35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
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180

185

190

Asn Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220

Gln His Thr
 225

<210> 132
 <211> 197
 <212> PRT
 <213> Rattus rattus

<400> 132

Met Val Ser Leu Pro Arg Leu Cys Ala Leu Trp Gly Cys Leu Leu Thr
 1 5 10 15

Ala Val His Leu Gly Gln Cys Val Thr Cys Ser Asp Lys Gln Tyr Leu
 20 25 30

His Asp Gly Gln Cys Cys Asp Leu Cys Gln Pro Gly Ser Arg Leu Thr
 35 40 45

Ser His Cys Thr Ala Leu Glu Lys Thr Gln Cys His Pro Cys Asp Ser
 50 55 60

Gly Glu Phe Ser Ala Gln Trp Asn Arg Glu Ile Arg Cys His Gln His
 65 70 75 80

Arg His Cys Glu Pro Asn Gln Gly Leu Arg Val Lys Lys Glu Gly Thr
 85 90 95

Ala Glu Ser Asp Thr Val Cys Thr Cys Lys Glu Gly Gln His Cys Thr
 100 105 110

Ser Lys Asp Cys Glu Ala Cys Ala Gln His Thr Pro Cys Ile Pro Gly
 115 120 125

Phe Gly Val Met Glu Met Ala Thr Glu Thr Thr Asp Thr Val Cys His
 130 135 140

Pro Cys Pro Val Gly Phe Phe Ser Asn Gln Ser Ser Leu Phe Glu Lys
 145 150 155 160

Cys Tyr Pro Trp Thr Ser Cys Glu Asp Lys Asn Leu Glu Val Leu Gln
 165 170 175

Lys Gly Thr Ser Gln Thr Asn Val Ile Cys Gly Leu Lys Ser Arg Met
 180 185 190

Arg Ala Leu Leu Val
195

<210> 133
<211> 208
<212> PRT
<213> Rattus rattus

<400> 133

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile
1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
50 55 60

Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
100 105 110

Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu
115 120 125

Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160

Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys
165 170 175

Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr
180 185 190

Gln Asn Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
195 200 205

<210> 134
<211> 224
<212> PRT

A-378CIP5.ST25.txt

<213> Rattus rattus

<400> 134

Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu
 1 5 10 15

Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys
 20 25 30

Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn
 35 40 45

Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys
 50 55 60

Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
 65 70 75 80

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
 85 90 95

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
 100 105 110

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
 115 120 125

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
 130 135 140

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
 145 150 155 160

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
 165 170 175

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
 180 185 190

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
 195 200 205

Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile
 210 215 220

<210> 135

<211> 205

<212> PRT

<213> Rattus rattus

<400> 135

Met Tyr Val Trp Val Gln Gln Pro Thr Ala Phe Leu Leu Leu Gly Leu
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1              5              10              15
Ser Leu Gly Val Thr Val Lys Leu Asn Cys Val Lys Asp Thr Tyr Pro
      20              25              30
Ser Gly His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val
      35              40              45
Ser Arg Cys Asp His Thr Arg Asp Thr Val Cys His Pro Cys Glu Pro
      50              55              60
Gly Phe Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr
      65              70              75
Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr Pro
      85              90              95
Thr Glu Asp Thr Val Cys Gln Cys Arg Pro Gly Thr Gln Pro Arg Gln
      100              105              110
Asp Ser Ser His Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly
      115              120              125
His Phe Ser Pro Gly Ser Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys
      130              135              140
Thr Leu Ser Gly Lys Gln Ile Arg His Pro Ala Ser Asn Ser Leu Asp
      145              150              155
Thr Val Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr
      165              170              175
Gln Arg Thr Thr Phe Arg Pro Thr Thr Val Pro Ser Thr Thr Val Trp
      180              185              190
Pro Arg Thr Ser Gln Leu Pro Ser Thr Pro Thr Leu Val
      195              200              205

```

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<210> 136
<211> 191
<212> PRT
<213> Rattus rattus

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<400> 136

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Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val
1              5              10              15
Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln
      20              25              30
Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
      35              40              45

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Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys
50 55 60

Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
65 70 75 80

His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
85 90 95

Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr
100 105 110

Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn
115 120 125

Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg
130 135 140

Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro
145 150 155 160

Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu
165 170 175

Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu
180 185 190

<210> 137
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 137
tatggatgaa gaaacttctc atcagctgct gtgtgataaa tgtccgccgg gtac

54

<210> 138
<211> 284
<212> PRT
<213> Mus musculus

<400> 138

Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser Gly Val Val Gln Ala
1 5 10 15

Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys Cys Pro Asp Gly Phe
20 25 30

Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys Ile Lys His Thr Asn
35 40 45

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Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys Gly Asn Ala Thr His
50 55 60

Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr Gln Lys Cys Gly Ile
65 70 75 80

Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr
85 90 95

Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val Asp Ser Leu Pro Gly
100 105 110

Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Arg His Ser
115 120 125

Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn
130 135 140

Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln Asp Ile Ala Leu Cys
145 150 155 160

Glu Ser Ser Val Gln Arg His Leu Gly His Ser Asn Leu Thr Thr Glu
165 170 175

Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly Lys Lys Ile Ser Pro
180 185 190

Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys Ser Ser Glu Gln Leu
195 200 205

Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr
210 215 220

Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu Lys Thr Ser His Phe
225 230 235 240

Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr Met Arg Phe Leu His
245 250 255

Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile
260 265 270

Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
275 280

<210> 139
<211> 380
<212> PRT
<213> Homo sapiens

<400> 139

A-378CIP5.ST25.txt

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His
 1 5 10 15
 Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His
 20 25 30
 Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr
 35 40 45
 Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro
 50 55 60
 Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His
 65 70 75 80
 Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe
 85 90 95
 Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala
 100 105 110
 Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe
 115 120 125
 Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
 130 135 140
 Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His
 145 150 155 160
 Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile
 165 170 175
 Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr
 180 185 190
 Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly
 195 200 205
 Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser
 210 215 220
 Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn
 225 230 235 240
 Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys
 245 250 255
 Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu
 260 265 270

A-378CIP5.ST25.txt

Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala
275 280 285

Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile
290 295 300

Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr
305 310 315 320

Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Lys His Phe
325 330 335

Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His
340 345 350

Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile
355 360 365

Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
370 375 380

<210> 140
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 140
tggaccaccc agaagtacct tcattatgac

30

<210> 141
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 141
gtcataatga aggtacttct ggggtggtcca

30

<210> 142
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 142
ggaccaccca gcttcattat gacgaagaaa c

31

<210> 143
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 143
gtttcttcgt cataatgaag ctgggtgggc c 31

<210> 144
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 144
gtggaccacc caggacgaag aaacctctc 29

<210> 145
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 145
gagaggtttc ttcgtcctgg gtggtccac 29

<210> 146
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 146
cgtttcctcc aaagttcctt cattatgac 29

<210> 147
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 147
gtcataatga aggaactttg gaggaaacg 29

<210> 148
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 148
ggaaacgttt cctgcaaagt accttcatta tg 32

<210> 149
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 149
 cataatgaag gtactttgca ggaaacgttt cc

32

<210> 150
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> muOPG

<400> 150
 cacgcaaaag tcgggaatag atgtcac

27

<210> 151
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> muOPG

<400> 151
 gtgacatcta ttcccgactt ttgcgtg

27

<210> 152
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> muOPG

<400> 152
 caccctgtcg gaagaggcct tcttc

25

<210> 153
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> muOPG

<400> 153
 gaagaaggcc tcttccgaca ggggtg

25

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> muOPG

<400> 154
tgacctctcg gaaagcagcg tgca 24

<210> 155
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> muOPG

<400> 155
tgcacgctgc tttccgagag gtca 24

<210> 156
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> muOPG

<400> 156
cctcgaaatc gagcgagcag ctcc 24

<210> 157
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> muOPG

<400> 157
cgatttcgag gtctttctcg ttctc 25

<210> 158
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> muOPG

<400> 158
ccgtgaaaat aagctcgta taactaggaa tgg 33

<210> 159
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> muOPG

<400> 159
ccattcctag ttataacgag cttattttca cgg 33

<210> 160
<211> 38
<212> DNA
<213> Artificial Sequence

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<220>
<223> muOPG

<400> 160
cctctgagct caagcttccg aggaccacaa tgaacaag 38

<210> 161
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> muOPG

<400> 161
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<210> 162
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> muOPG

<400> 162
cctctgagct caagcttccg aggaccacaa tgaacaag 38

<210> 163
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> muOPG

<400> 163
cctctctcga gtcaaggaac agcaaacctg aagaaggc 38

<210> 164
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> muOPG

<400> 164
cctctgagct caagcttccg aggaccacaa tgaacaag 38

<210> 165
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> muOPG

<400> 165
cctctctcga gtcactctgt ggtgagggtc gagtggcc 38

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<210> 166
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> muOPG

<400> 166
 cctctgagct caagcttccg aggaccacaa tgaacaag 38

<210> 167
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> muOPG

<400> 167
 cctctctcga gtcaggatgt tttcaagtgc ttgagggc 38

Sub 39

<210> 168
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> pAMG22

<400> 168
 Met Lys His His His His His His His Ala Ser Val Asn Ala Leu Glu
 1 5 10 15